# - 34 35 SEQUENCE LISTING

#### (1) GENERAL INFORMATION:

- (i) APPLICANT: Papayannopoulou, Thalia (USA only)
  Board of Regents, U.
  Washington (except USA)
- (ii) TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM CELLS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: c/o FISH & NEAVE
  - (B) STREET: 1251 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10020
- (V) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/977,702
  - (B) FILING DATE: 13-NOV-1992
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Haley Jr., James F.
  - (B) REGISTRATION NUMBER: 27,794
  - (C) REFERENCE/DOCKET NUMBER: B173CIP
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (212) 596-9000
    - (B) TELEFAX: (212) 596-9090
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 360 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(350)



GTCAAACTGC AGCAGTCTGG GGCAGAGCTT GTGAAGCCAG GGGCCTCAGT CAAGTTGTCC 60

TGCACAGCTT CTGGCTTCAA CATTAAAGAC ACCTATATGC ACTGGGTGAA GCAGAGGCCT 120

GAACAGGGCC TGGAGTGGAT TGGAAGGATT GATCCTGCGA GTGGCGATAC TAAATATGAC 180

CCGAAGTTCC AGGTCAAGGC CACTATTACA GCGGACACGT CCTCCAACAC AGCCTGGCTG 240

CAGCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTACT ACTGTGCAGA CGGAATGTGG 300

GTATCAACGG GATATGCTCT GGACTTCTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA 360

#### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTATTGTGA TGACCCAGAC TCCCAAATTC CTGCTTGTTT CAGCAGGAGA CAGGGTTACC 60

ATAACCTGCA AGGCCAGTCA GAGTGTGACT AATGATGTAG CTTGGTACCA ACAGAAGCCA 120

GGGCAGTCTC CTAAACTGCT GATATATTAT GCATCCAATC GCTACACTGG AGTCCCTGAT 180

CGCTTCACTG GCAGTGGATA TGGGACGGAT TTCACTTTCA CCATCAGCAC TGTGCAGGCT 240

GAAGACCTGG CAGTTTATTT CTGTCAGCAG GATTATAGCT CTCCGTACAC GTTCGGAGGG 300

GGGACCAAGC TGGAGATC 318

#### (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid



48

- 38 <del>-</del> 37

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

# (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..57

# (ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 58..429

# (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

#### (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pMDR1019 insert: Stage 1 heavy chain variable region"

ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	Gly	Pro -5	Ala	Val	Ala	Leu	Leu -10	Cys	Phe	Val	Arg	Trp -15	Thr	Trp	Asp	Met -19
96	AGA	GTG	CTT	GGT	CCA	GGT	AGC	GAG	CAG	CTG	CAA	GTC	CAG	TCC	CAC	GCC
	Arg	Val	Leu	Gly 10	Pro	Gly	Ser	Glu	Gln 5	Leu	Gln	Val	Gln 1	Ser	His	Ala
144	ATT	AAC	TTC	GGC	TCT	GTG	ACC	TGC	ACC	CTG	AGC	CTG	ACC	CAG	AGC	CCT
	Ile	Asn	Phe	Gly	Ser 25	Val	Thr	Cys	Thr	Leu 20	Ser	Leu	Thr	Gln	Ser 15	Pro
192	CTT	GGT	CGA	GGA	CCT	CCA	CAG	AGA	GTG	TGG	CAC	ATG	TAT	ACC	GAC	AAA
	Leu 45	Gly	Arg	Gly	Pro	Pro 40	Gln	Arg	Val	Trp	His 35	Met	Tyr	Thr	Asp	Lys 30
240	GAC	TAT	AAA	ACT	GAT	GGC	AGT	GCG	CCT	GAT	ATT	AGG	GGA	ATT	TGG	GAG
	Asp	Туг 60	Lys	Thr	Asp	Gly	Ser 55	Ala	Pro	Asp	Ile	Arg 50	Gly	Ile	Trp	Glu
288	AAC	AAG	AGC	ACC	GAC	GTA	CTG	ATG	ACA	GTG	AGA	GTC	CAG	TTC	AAG	CCG
	Asn	Lys	Ser 75	Thr	Asp	Val	Leu	Met 70	Thr	Val	Arg	Val	Gln 65	Phe	Lys	Pro
336	GTC	GCG	ACC	GAC	GCC	GCC	ACA	GTG	AGC	AGC	CTC	AGA	CTG	AGC	TTC	CAG
	Val	Ala	Thr	Asp	Ala	Ala	Thr	Val	Ser	Ser	Leu	Arg	Leu	Ser	Phe	Gln

3

- 37 -38

80

TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC

TYR TYR Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp 100 105

TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser 110 120

85

#### (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 143 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-19 -15 -10 -5

Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg

1 5 10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile 15 20 25

Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30 35 40 45

Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
50 55 60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn 65 70 75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val 80 85 90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp 95 100 105

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser 110 120

#### (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs

48

- 389

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

#### (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..57

# (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..384

# (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

# (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBag190 insert: VK1 (DQL) light chain variable region"

ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met -19	Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Phe	Leu -10	Val	Ala	Thr	Ala	Thr -5	Gly	
GTT	CAC	TCC	GAC	ATC	CAG	CTG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
Val	His	Ser	Asp 1	Ile	Gln	Leu	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AGT	GTG	144
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	Ala 25	Ser	Gln	Ser	Val	
ACT	AAT	GAT	GTA	GCT	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	192
Thr 30	Asn	Asp	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
CTG	CTG	ATC	TAC	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGT	GTG	CCA	AGC	AGA	240
Leu	Leu	Ile	Tyr	Tyr 50	Ala	Ser	Asn	Arg	Tyr 55	Thr	Gly	Val	Pro	Ser 60	Arg	
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	<b>Asp</b> 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser	
CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAG	GAT	TAT	AGC	336



WO 94/11027

384

- 39uō

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser 80 85 90

TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys 95 100 105

TG 386

#### (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val 15 20 25

Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser 80 85 90

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys 95 100 105

# (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear



- 40 -41

(ix)	FEATURE	:
------	---------	---

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..57

#### (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 58..429

# (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..429

# (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG195 insert: AS heavy chain variable region"

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG	GAC	TGG	ACC	TGG	AGG	GTC	TTC	TGC	TTG	CTG	GCT	GTA	GCA	CCA	GGT	48
Met -19	Asp	Trp	Thr	Trp -15	Arg	Val	Phe	Cys	Leu -10	Leu	Ala	Val	Ala	Pro -5	Gly	
GCC	CAC	TCC	CAG	GTC	CAA	CTG	CAG	GAG	AGC	GGT	CCA	GGT	CTT	G <b>TG</b>	AGA	96
Ala	His	Ser	Gln 1	Val	Gln	Leu	Gln 5	Glu	Ser	Gly	Pro	Gly 10	Leu	Val	Arg	
CCT	AGC	CAG	ACC	CTG	AGC	CTG	ACC	TGC	ACC	GCG	TCT	GGC	TTC	AAC	ATT	144
Pro	Ser 15	Gln	Thr	Leu	Ser	Leu 20	Thr	Cys	Thr	Ala	Ser 25	Gly	Phe	Asn	Ile	
AAA	GAC	ACC	TAT	ATG	CAC	TGG	GTG	AGA	CAG	CCA	CCT	GGA	CGA	GGT	CTT	192
Lys 30	Asp	Thr	Tyr	Met	His 35	Trp	Val	Arg	Gln	Pro 40	Pro	Gly	Arg	Gly	Leu 45	
GAG	TGG	ATT	GGA	AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	240
Glu	Trp	Ile	Gly	Arg 50	Ile	Asp	Pro	Ala	Ser 55	Gly	Asp	Thr	Lys	Tyr 60	Asp	
CCG	AAG	TTC	CAG	GTC	AGA	GTG	ACA	ATG	CTG	GTA	GAC	ACC	AGC	AGC	AAC	288
Pro	Lys	Phe	Gln 65	Val	Arg	Val	Thr	Met 70	Leu	Val	Asp	Thr	Ser 75	Ser	Asn	
CAG	TTC	AGC	CTG	AGA	CTC	AGC	AGC	GTG	ACA	GCC	GCC	GAC	ACC	GCG	GTC	336
Gln	Phe	Ser 80	Leu	Arg	Leu	Ser	Ser 85	Val	Thr	Ala	Ala	Asp 90	Thr	Ala	Val	

41



TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp 100 ... 105

TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 143 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-19 -15 -10 -5

Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
1 5 10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile 15 20 25

Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu 30 45

Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
50 55 60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn 65 70 75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val 80 85 90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp 95 100 105

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser 110 120

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:

W2

•

- 42 -43

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

#### (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..57

#### (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..384

# (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

#### (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG198 insert VK2 (SVMDY) light chain variable region"

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	GGT	TGG	TCC	TGC	ATC	ATC	CTG	TTC	CTG	GTT	GCT	ACC	GCT	ACC	GGT	48
Met -19	Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Phe	Leu -10	Val	Ala	Thr	Ala	Thr -5	Gly	
GTC	CAC	TCC	AGC	ATC	GTG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
Val	His	Ser	Ser 1	Ile	Val	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AGT	GTG	144
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	Ala 25	Ser	Gln	Ser	Val	
ACT	AAT	GAT	GTA	GCT	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	192
Thr 30	Asn	Asp	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
CTG	CTG	ATC	TAC	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGT	GTG	CCA	GAT	AGA	240
Leu	Leu	Ile	Tyr	Tyr 50	Ala	Ser	Asn	Arg	Tyr 55	Thr	Gly	Val	Pro	Asp 60	Arg	
TTC	AGC	GGT	AGC	GGT	TAT	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser 65	Gly	Tyr	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser	



TG

386



# - 43 - 44

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC 336

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser 80

TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys 95

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val 15 20 25

Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
50 55 60

Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser 80 85 90

Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys 95 100 105

HY